

Qy	241	RNPDSRALIREKLTADPDSEVATTSLRVSLMCPLGKMRLTVPCCALTCAHLQSFDAALY	300
Db	295	RNPDSRALIREKLTADPDSEVATTSLRVSLMCPLGKMRLTVPCCALTCAHLQSFDAALY	354
Qy	301	LQNNKKPTWTCEVCDKKAIPYESLIIDGLFMEILSSCSDCDEIQFMEDGSCWCMKPCKEA	360
Db	355	LQNNKKPTWTCEVCDKKAIPYESLIIDGLFMEILSSCSDCDEIQFMEDGSCWCMKPCKEA	414
Qy	361	SEVCPPPGYGLDGLQYSVPCGDPSSENKKYEVIDLTTIESSSDEDELPTTKHKCVTSAA	420
Db	415	SEVCPPPGYGLDGLQYSVPCGDPSSENKKYEVIDLTTIESSSDEDELPTTKHKCVTSAA	474
Qy	421	IPALPGSKGVLTSGHQSPSVLRSPAMGTGGDFLSLLPHHEYPPAPFLGADIQGDLFSF	480
Db	475	IPALPGSKGVLTSGHQSPSVLRSPAMGTGGDFLSLLPHHEYPPAPFLGADIQGDLFSF	534
Qy	481	LQTESQHYPGSVITSLDEQDALGHFFOYRGTPSFHPLAFTPLATLGSSHCSATPAPPGRVS	540
Db	535	LQTESQHYPGSVITSLDEQDALGHFFOYRGTPSFHPLAFTPLATLGSSHCSATPAPPGRVS	594
Qy	541	SIVAPGALREHGCGPIFPSGSLTGCRSDIIISLD	574
Db	595	SIVAPGALREHGCGPIFPSGSLTGCRSDIIISLD	628

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Query Match	100.0%;	Score 3056;	DB 4;	Length 628;
Best Local Similarity	100.0%;	Pred. No. 2.2e-272;		
Matches 574;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKIKELYYRRFFPKRTTGLGSPDLSLLSLPPGTSPVGSPPGLAPIPPTTLAPGTLGPKEVD	60	
Db	55	MKIKELYYRRFFPKRTTGLGSPDLSLLSLPPGTSPVGSPPGLAPIPPTTLAPGTLGPKEVD	114	
QY	61	MHPPLQPQVHPDVMTKLPPEVYVGELIRTTTLASTSSQRFEAAHFTFALTPOOVQIILT	120	
Db	115	MHPPLQPQVHPDVMTKLPPEVYVGELIRTTTLASTSSQRFEAAHFTFALTPOOVQIILT	174	
QY	121	SREVLPGAACDYIIQVLRFLCLETSCPDIEDYFPNNLFVKNGKICPLPGVLPTKNAG	180	
Db	175	SREVLPGAACDYIIQVLRFLCLETSCPDIEDYFPNNLFVKNGKICPLPGVLPTKNAG	234	
QY	181	PKRPSRPINITPIARLSATVENTIVNWSSEFGRNYSLVYLVRQLTAGTLLQKLRAKGI	240	
Db	235	PKRPSRPINITPIARLSATVENTIVNWSSEFGRNYSLVYLVRQLTAGTLLQKLRAKGI	294	
QY	241	RNPDSRALIKEKLTADDPDEVAATTSLRVSLMCPLGKORLTVFCRALTCALHQSFDAALY	300	
Db	295	RNPDSRALIKEKLTADDPDEVAATTSLRVSLMCPLGKORLTVFCRALTCALHQSFDAALY	354	

Qy	301	LQNNKPTWTCTPCVCDKAPYESI	I	DGLFMELI	SSCSDCEIQFMDGSCWCMKPKKXA	360
Db	355	LQNNKPTWTCTPCVCDKAPYESI	I	DGLFMELI	SSCSDCEIQFMDGSCWCMKPKKXA	414
Qy	361	SEVCPPGYGLDGLQYSPVQGGDSENNK	KEVE	IDLTI	ESSDREDLPTTKHCSVTGAA	420
Db	415	SEVCPPGYGLDGLQYSPVQGGDSENNK	KEVE	IDLTI	ESSDREDLPTTKHCSVTGAA	474
Qy	421	IPALPGSKGWLVTSGHQSSVLRS	PAMGTLGGDFT	SSPL	PHYPAFLGADIQGLDLFSF	480
Db	475	IPALPGSKGWLVTSGHQSSVLRS	PAMGTLGGDFT	SSPL	PHYPAFLGADIQGLDLFSF	534
Qy	481	LQTESQHYGFSVITSLDEQALGHFFQY	RGTPSHFLG	LAPL	TGSSHCSCATPAPPGRVS	540
Db	535	LQTESQHYGFSVITSLDEQALGHFFQY	RGTPSHFLG	LAPL	TGSSHCSCATPAPPGRVS	594
Qy	541	SI	VAPGALREHGGLPSG	PSLTGCRSDI	ISLD	574
Db	595	SI	VAPGALREHGGLPSG	PSLTGCRSDI	ISLD	628

RESULT 5
 US-09-062-440-2
 Sequence 2, Application US/09062440
 Patent No. 6207422
 GENERAL INFORMATION:
 APPLICANT: Brown, Arthur M.
 APPLICANT: Yang, Qing
 APPLICANT: Wible, Barbara A.
 TITLE OF INVENTION: A Protein that Enhances Expression of
 POTASSIUM CHANNELS on Cell Surfaces
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESS: Calfee, Halter & Griswold LLP
 STREET: 1400 McDonald Investment Center, 800 Superior
 STREET: Avenue
 CITY: Cleveland
 STATE: Ohio
 COUNTRY: US
 ZIP: 44114
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/062,440
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Docherty, Pamela A.
 REGISTRATION NUMBER: 40591
 REFERENCE/DOCKET NUMBER: 22884/04004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 2166228200
 TELEFAX: 2162410816
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 574 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-062-440-2

	Query Match	96.3%	Score 2944;	DB 3;	Length 574;
	Best Local Similarity	96.3%;	Pred. No. 3.9e-262;		
	Matches 553;	Conservative	7;	Mismatches 14;	Indels 0;
					Gaps 0;
QY	1	MKIKELRRRFRKRTIGPSDLSLLSPPTSPVGSFGLPIPTTLATGTLGPKREVD	60		
Db	1	MKIKELRRRFRKRTIGPSDLSLLSPPTSPVGSFGLPIPTTLATGTLGPKREVD	60		
QY	61	MHPPLPQPVHPDVTWKPLPFYEVYIGELIRPTTLASTSSORFEEAHFTFALTPOCVQOILT	120		

Db 61 MHPPLPQVHPDVTKMPLFFVEVYGGELIRPTTLASTSSQRFEEAHFTALTPOOQOILT 120
QY 121 SREVLPGAKCDYTIQVQLRFLCFCETSCPOEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 180
Db 121 SREVLPGAKCDYTIQVQLRFLCFCETSCPOEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 180
QY 181 PKRPSRPINTPLARLSATVNTIVVWMSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 240
Db 181 PKRPSRPINTPLARLSATVNTIVVWMSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 240
QY 241 RNPDSRALIKEKLTADPDSVATTSLRVSLMCPGKMLTVPCCALTCALHQSFDAAALY 300
Db 241 RNPDSRALIKEKLTADPDSVATTSLRVSLMCPGKMLTVPCCALTCALHQSFDAAALY 300
QY 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCPMKPKKEA 360
Db 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCPMKPKKEA 360
QY 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEVDLTIESSEDDEDLPTTKHCSVTSAA 420
Db 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEVDLTIESSEDDEDLPTTKHCSVTSAA 420
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QY 481 LQTESQHYGPSVITSLDEQDALGHFFQYRGTPSHFLGAPLPTLGSSHCSATPAPPGRVS 540
Db 481 LQTESQHYGPSVITSLDEQDALGHFFQYRGTPSHFLGAPLPTLGSSHCSATPAPPGRVS 540
QY 541 SIVAPGGALREHGGLPSPGSLTGCRSDIISLD 574
Db 541 SIVAPGGALREHGGLPSPGSLTGCRSDIISLD 574

RESULT 6
US-09-712-495-2
; Sequence 2, Application US/09712495
; Patent No. 6391561
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur
; APPLICANT: Wible, Barbara
; APPLICANT: Yang, Qing
; TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell Sur
; FILE REFERENCE: 22884/04046
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US/09/712,495
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-712-495-2

Query Match 96.3%; Score 2944; DB 4; Length 574;
Best Local Similarity 96.3%; Pred. No. 3,9e-262;
Matches 553; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKIKELYRFRFRKTLGSDLSLLPPTGTSVPGSPGLPIAPPILLAGTLLGPKREV 60
Db 1 MKIKELYRFRFRKTLGSDLSLLPPTGTSVPGSPGLPIAPPILLAGTLLGPKREV 60
QY 61 MHPPLPQVHPDVTKMPLFFVEVYGGELIRPTTLASTSSQRFEEAHFTALTPOOQOILT 120
Db 61 MHPPLPQVHPDVTKMPLFFVEVYGGELIRPTTLASTSSQRFEEAHFTALTPOOQOILT 120
QY 121 SREVLPGAKCDYTIQVQLRFLCFCETSCPOEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 180

Db 121 SREVLPGAKCDYTIQVQLRFLCFCETSCPOEDYFPPNLFVKVNGKLCPLPGYLPPTKNGAE 180
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Db 181 PKRPSRPINTPLARLSATVNTIVVWMSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 240
QY 241 RNPDSRALIKEKLTADPDSVATTSLRVSLMCPGKMLTVPCCALTCALHQSFDAAALY 300
Db 241 RNPDSRALIKEKLTADPDSVATTSLRVSLMCPGKMLTVPCCALTCALHQSFDAAALY 300
QY 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCPMKPKKEA 360
Db 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCPMKPKKEA 360
QY 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEVDLTIESSEDDEDLPTTKHCSVTSAA 420
Db 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEVDLTIESSEDDEDLPTTKHCSVTSAA 420
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Db 421 IPALPGSGKGLTSGHQPSSVLRSPAMGTGDLGDFLSSLPHEYPFPAFLGADIQGLDLFSF 480
QY 481 LQTESQHYGPSVITSLDEQDALGHFFQYRGTPSHFLGAPLPTLGSSHCSATPAPPGRVS 540
Db 481 LQTESQHYGPSVITSLDEQDALGHFFQYRGTPSHFLGAPLPTLGSSHCSATPAPPGRVS 540
QY 541 SIVAPGGALREHGGLPSPGSLTGCRSDIISLD 574
Db 541 SIVAPGGALREHGGLPSPGSLTGCRSDIISLD 574

RESULT 7
US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 216228200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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; CURRENT APPLICATION NUMBER: US/09/286,132
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2667068
US-09-286-132-2

Query Match      100.0%   Score 544; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPCVCDKKAPYBSLIIDGLFMELSSCDSDCDEIQFMEDGSGWCPMKPKKEASEVCPPPG 60
Db 363 TWTCPCVCDKKAPYBSLIIDGLFMELSSCDSDCDEIQFMEDGSGWCPMKPKKEASEVCPPPG 422
QY 61 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 99
Db 423 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 461

RESULT 6
US-09-836-941-2
; Sequence 2, Application US/09836941
; Patent No. 6465200.
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2667068
US-09-836-941-2

Query Match      100.0%   Score 544; DB 4; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPCVCDKKAPYBSLIIDGLFMELSSCDSDCDEIQFMEDGSGWCPMKPKKEASEVCPPPG 60
Db 363 TWTCPCVCDKKAPYBSLIIDGLFMELSSCDSDCDEIQFMEDGSGWCPMKPKKEASEVCPPPG 422
QY 61 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 99
Db 423 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 461

RESULT 7
US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATA:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Doherly, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2166224200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; NAME/KEY: Peptide
; LOCATION: 37..38
; OTHER INFORMATION: /note= "glycine or serine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 41..42
; OTHER INFORMATION: /note= "proline or serine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 48..49
; OTHER INFORMATION: /note= "alanine or threonine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 115..116
; OTHER INFORMATION: /note= "valine or leucine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 335..336
; OTHER INFORMATION: /note= "serine or asparagine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 381..382
; OTHER INFORMATION: /note= "glycine or glutamic acid"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 383..384
; OTHER INFORMATION: /note= "aspartic acid or
; OTHER INFORMATION: asparagine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 384..385
; OTHER INFORMATION: /note= "isoproline or glutamine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 390..391
; OTHER INFORMATION: /note= "lysine or arginine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 416..417
; OTHER INFORMATION: /note= "serine or proline"
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FEATURE:
NAME/KEY: Peptide
LOCATION: 431..432
OTHER INFORMATION: /note= "valine or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 489..490
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 501..502
OTHER INFORMATION: /note= "alanine or threonine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 508..509
OTHER INFORMATION: /note= "tyrosine or phenylalanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 513..514
OTHER INFORMATION: /note= "serine or proline"
FEATURE:
NAME/KEY: Peptide
LOCATION: 528..529
OTHER INFORMATION: /note= "cysteine or arginine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 535..536
OTHER INFORMATION: /note= "proline or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 547..548
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 548..549
OTHER INFORMATION: /note= "alanine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 570..571
OTHER INFORMATION: /note= "isoleucine or valine"
US-09-062-440-6

Query Match 95.6%; Score 520; DB 3; Length 574;
Best Local Similarity 96.0%; Pred. No. 1.2e-51;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYSLIIDGLFMEILSSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DB 309 TWTCPVCDKAPYSLIIDGLFMEILSSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 368
QY 61 YGLDGLQVSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99
DB 369 YGLDGLQVSPVQGGPSENKKKVEVIDLTIESSSDEEDL 407

RESULT 8
US-09-062-440-7
Sequence 7, Application US/09062440
Patent No. 6207422

GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Wang, Qing
TITLE OF INVENTION: A Protein that Enhances Expression of Potassium Channels on Cell Surfaces
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior

STREET: Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062.440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884.04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2162228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-062-440-7

Query Match 95.0%; Score 517; DB 3; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.8e-52;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 TWTCPVCDKAPYSLIIDGLFMEILSSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DB 1 TWTCPVCDKAPYSLIIDGLFMEILSSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
QY 61 YGLDGLQVSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99
DB 61 YGLDGLQVSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99

RESULT 9
US-09-742-495-7
Sequence 7, Application US/09712495
Patent No. 6391561

GENERAL INFORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Wang, Qing
TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell Surfaces
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 22884.04046
CURRENT APPLICATION NUMBER: US/09/712.495
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/062.440
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent In version 3.0
SEQ ID NO 7

LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-09-712-495-7

Query Match 95.0%; Score 517; DB 4; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.8e-52;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYSLIIDGLFMEILSSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60

QY 61 MHPPLQPVHDPVTKMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOOXQOILT 120
DB 78 -----PVHPDVTMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOOXQOILT 130
QY 121 SREVLPQAKLDYTIQVLRFLCETSLPQEDYFPNLFVKVNGKLCPLPGYLPPTKNGAE 180
DB 131 SREVLPQAKLDYTIQVLRFLCETSLPQEDYFPNLFVKVNGKLCPLPGYLPPTKNGAE 190
QY 181 PKRP-----SRPINITPKARLSATVPNTIIVNWSSEFGNTSLSVLVRQLTAG 229
DB 191 PRGPAVRSTSHPWLDSPQSPPTP-----SLIGHLSLDG--ITPCPCLVRQLTAG 238
QY 230 TLQKLRAGIRNPDHRSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRAITC 289
DB 239 TLQKLRAGIRNPDHRSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRAITC 298
QY 290 AHLQSFSAALYLQWNE-KPTWTCPVCDKAPWESLIIDGLFMEILXSCSDCDEIQFMEDG 348
DB 299 AHLQSFDAALYLQWNEKPTWTCPVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDG 358
QY 349 STCPMPKKEASEVCPGPGGLDGLQYSPVQXGKPSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 408
DB 359 SWCPMPKKEASEVCPGPGGLDGLQYSAVQEGIQPESKRVVIDLTIESSSDEEDLPP 418
QY 409 TKKHCVTSAAIPALPGSKGLTSGHQPSSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 468
DB 419 TKKHCVTSAAIPALPGSKGLTSGHQPSSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 478
QY 469 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLGHFFQXRFTHXFLGLPLAFTLGSXHS 527
DB 479 ADIQGLDLFSLQTESQYXPSVITSLDEQDLGHFFQXRFTHXFLGLPLAFTLGSXHS 538
QY 528 ATPAPXGRVSSIVAPGXLRGEGGLPSPGSLTGCSDIXSLD 572
DB 539 STAPPXGRVSSIVAPGXLRGEGGLPSPGSLTGCSDIXSLD 583

RESULT 10

US-09-836-941-17
; Sequence 17, Application US/09836941
; Patent No. 6465200
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: 92689028
US-09-836-941-17

Query Match 78.7%; Score 2317; DB 4; Length 583;
Best Local Similarity 79.0%; Pred. No. 1.5e-221;
Matches 462; Conservative 14; Mismatches 49; Indels 60; Gaps 6;

QY 1 MKIKELVRRFRPKTLGSDLSLSPGTSVPGSPXPLAXIPPTLLXPGTLGPKREVD 60
DB 46 MKIKELVRRFRPKTLGSDLSLSPGTSVPGSPXPLAXIPPTLLXPGTLGPKREVD 77
QY 61 MHPPLQPVHDPVTKMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOOXQOILT 120
DB 78 -----PVHPDVTMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOOXQOILT 130
QY 121 SREVLPQAKLDYTIQVLRFLCETSLPQEDYFPNLFVKVNGKLCPLPGYLPPTKNGAE 180

DB 131 SREVLPQAKLDYTIQVLRFLCETSLPQEDYFPNLFVKVNGKLCPLPGYLPPTKNGAE 190
QY 181 PKRP-----SRPINITPKARLSATVPNTIIVNWSSEFGNTSLSVLVRQLTAG 229
DB 191 PRGPAVRSTSHPWLDSPQSPPTP-----SLIGHLSLDG--ITPCPCLVRQLTAG 238
QY 230 TLQKLRAGIRNPDHRSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRAITC 289
DB 239 TLQKLRAGIRNPDHRSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRAITC 298
QY 290 AHLQSFSAALYLQWNE-KPTWTCPVCDKAPWESLIIDGLFMEILXSCSDCDEIQFMEDG 348
DB 299 AHLQSFDAALYLQWNEKPTWTCPVCDKAPYESLIIDGLFMEILNCSDCDEIQFMEDG 358
QY 349 STCPMPKKEASEVCPGPGGLDGLQYSPVQXGKPSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 408
DB 359 SWCPMPKKEASEVCPGPGGLDGLQYSAVQEGIQPESKRVVIDLTIESSSDEEDLPP 418
QY 409 TKKHCVTSAAIPALPGSKGLTSGHQPSSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 468
DB 419 TKKHCVTSAAIPALPGSKGLTSGHQPSSVLRSPAMGTGLXDFLSLPLHYPAPPPLG 478
QY 469 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLGHFFQXRFTHXFLGLPLAFTLGSXHS 527
DB 479 ADIQGLDLFSLQTESQYXPSVITSLDEQDLGHFFQXRFTHXFLGLPLAFTLGSXHS 538
QY 528 ATPAPXGRVSSIVAPGXLRGEGGLPSPGSLTGCSDIXSLD 572
DB 539 STAPPXGRVSSIVAPGXLRGEGGLPSPGSLTGCSDIXSLD 583

RESULT 11

US-08-399-696-102
; Sequence 102, Application US/08399696
; Patent No. 5756669
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,696
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,671
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15522-000710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-399-696-102

Query Match 50.3%; Score 1480.5; DB 1; Length 597;
Best Local Similarity 53.1%; Pred. No. 2.3e-138;
Matches 326; Conservative 77; Mismatches 152; Indels 59; Gaps 19;

1 CURRENT FILING DATE: 2001-04-17
2 PRIOR APPLICATION NUMBER: 09/286,132
3 PRIOR FILING DATE: 1999-04-01
4 NUMBER OF SEQ ID NOS: 17
5 SOFTWARE: PERL Program
6 SEQ ID NO 17
7 LENGTH: 583
8 TYPE: PRT
9 ORGANISM: Mus musculus
10 FEATURE: -
11 OTHER INFORMATION: 92689028
12 US-09-836-941-17

Query Match 95.0%; Score 516; DB 4; Length 583;
Best Local Similarity 96.0%; Pred. No. 1.1e-52;
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TWTCPCDKKAPYESLIIDGLFMEILNSCSDCDIQFMEDGSCWCPMKPKKEASEVCPPPG 60
Db 318 TWTCPCDKKAPYESLIIDGLFMEILNSCSDCDIQFMEDGSCWCPMKPKKEASEVCPPPG 377
Qy 61 YGLDGLQYSPVOENQSGNKKRVEIDLTIESSDDEDL 99
Db 378 YGLDGLQYSAVQEGIQPKESKKRVEIDLTIESSDDEDL 416

RESULT 13

US-09-062-440-6
Sequence 6, Application US/09062440
Patent No. 6207422
GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Qing
APPLICANT: Noble, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/062,440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884/04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 37..38

OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 41..42
OTHER INFORMATION: /note= "proline or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 48..49
OTHER INFORMATION: /note= "alanine or threonine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 115..116
OTHER INFORMATION: /note= "valine or leucine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 335..336
OTHER INFORMATION: /note= "serine or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 381..382
OTHER INFORMATION: /note= "glycine or glutamic acid"
FEATURE:
NAME/KEY: Peptide
LOCATION: 383..384
OTHER INFORMATION: /note= "aspartic acid or
asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 384..385
OTHER INFORMATION: /note= "isoproline or glutamine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 390..391
OTHER INFORMATION: /note= "lysine or arginine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 416..417
OTHER INFORMATION: /note= "serine or proline"
FEATURE:
NAME/KEY: Peptide
LOCATION: 431..432
OTHER INFORMATION: /note= "valine or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 489..490
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 501..502
OTHER INFORMATION: /note= "alanine or threonine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 508..509
OTHER INFORMATION: /note= "tyrosine or phenylalanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 513..514
OTHER INFORMATION: /note= "serine or proline"
FEATURE:
NAME/KEY: Peptide
LOCATION: 528..529
OTHER INFORMATION: /note= "cysteine or arginine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 535..536
OTHER INFORMATION: /note= "proline or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 547..548

OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 548..549
OTHER INFORMATION: /note= "alanine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 570..571
OTHER INFORMATION: /note= "isoleucine or valine"
US-09-062-440-6

Query Match 94.1%; Score 511; DB 3; Length 574;
Best Local Similarity 94.9%; Pred. No. 4.3e-52;
Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TWCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 60
DB 309 TWCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 368
QY 61 YLDGLQYSPVOEGNQSENKKEVEVIDLTIESSSDEEDL 99
DB 369 YLDGLQYSPVOEGNQSENKKEVEVIDLTIESSSDEEDL 407

RESULT 14
US-09-062-440-10
Sequence 10, Application US/09062440
Patent No. 6207422
GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Qing
APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884/04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not-relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 25..26
OTHER INFORMATION: /note= "serine or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 61..62

OTHER INFORMATION: /note= "glycine or glutamic acid"
FEATURE:
NAME/KEY: Peptide
LOCATION: 63..64
OTHER INFORMATION: /note= "aspartic acid or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 64..65
OTHER INFORMATION: /note= "proline or glutamine"
NAME/KEY: Peptide
LOCATION: 70..71
OTHER INFORMATION: /note= "lysine or arginine"
US-09-062-440-10

Query Match 93.2%; Score 506; DB 3; Length 98;
Best Local Similarity 94.9%; Pred. No. 1.6e-52;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 61
DB 1 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 60
QY 62 GLDGLQYSPVOEGNQSENKKEVEVIDLTIESSSDEEDL 99
DB 61 GLDGLQYSPVOEGNQSENKKEVEVIDLTIESSSDEEDL 98

RESULT 15
US-09-712-495-10
Sequence 10, Application US/09712495
Patent No. 6391561
GENERAL INFORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Wible, Barbara
APPLICANT: Yang, Qing
TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 22884/04046
CURRENT APPLICATION NUMBER: US/09/712,495
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/062,440
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in version 3.0
SEQ ID NO 10
LENGTH: 98
TYPE: PRT
FEATURE:
ORGANISM: synthetic construct
NAME/KEY: misc_feature
LOCATION: (25)..(25)
OTHER INFORMATION: Xaa = serine-or asparagine
NAME/KEY: misc_feature
LOCATION: (61)..(61)
OTHER INFORMATION: Xaa = glycine or glutamic acid
NAME/KEY: misc_feature
LOCATION: (63)..(63)
OTHER INFORMATION: Xaa = aspartic acid or asparagine
NAME/KEY: misc_feature
LOCATION: (64)..(64)
OTHER INFORMATION: Xaa = proline or glutamine
US-09-712-495-10

Query Match 91.3%; Score 496; DB 4; Length 98;
Best Local Similarity 93.9%; Pred. No. 2.5e-51;
Matches 92; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 61
DB 1 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPDPG 60

Db 370 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 407

RESULT 5
US-09-712-495-4
; Sequence 4, Application US/09712495
; Patent No. 6391561
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur
; APPLICANT: Wible, Barbara
; APPLICANT: Yang, Qing
; TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell Surfaces
; TITLE OF INVENTION: and Nucleic Acids That Encode The Same
; FILE REFERENCE: 22884/04046
; CURRENT APPLICATION NUMBER: US/09/712,495
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 09/062,440
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-495-4

Query Match 97.7%; Score 505; DB 4; Length 574;
Best Local Similarity 94.9%; Pred. No. 1.7e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 60
Db 310 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 369
Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 98
Db 370 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 407

RESULT 6
US-09-286-132-2
; Sequence 2, Application US/09286132
; Patent No. 6242185
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/286,132
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2667068
US-09-286-132-2

Query Match 97.7%; Score 505; DB 3; Length 628;
Best Local Similarity 94.9%; Pred. No. 1.9e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 60
Db 364 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 423
Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 98
Db 424 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 461

RESULT 7
US-09-836-941-2
; Sequence 2, Application US/09836941
; Patent No. 6465200
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2667068
US-09-836-941-2

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Best Local Similarity 94.9%; Pred. No. 1.9e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 98
Db 424 GLDGLQSPVQGGPSENKKKVEIDLTIESSDEEDL 461

RESULT 8
US-09-062-440-10
; Sequence 10, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/062,440
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 216228200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 10:

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; SEQUENCE CHARACTERISTICS:
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; OTHER INFORMATION: /note= "proline or glutamine"
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; US-09-062-440-10
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; Query Match 97.5%; Score 504; DB 3; Length 98;
; Best Local Similarity 99.0%; Pred. No. 2.3e-54;
; Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 WTCPCVCDKAPYESIIDGLFNEILXSCSDCEIQMEDGSLPMKPKKEASEVCPFGY 60
QY 61 GLDGLQYSPVQXGXPSENKXVEVDLTIESSSDEEDL 98
DB 61 GLDGLQYSPVQXGXPSENKXVEVDLTIESSSDEEDL 98
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RESULT 9
US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
;
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 21622828200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
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; STRANDEDNESS: not relevant
; TOPOLOGY: linear
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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.8056 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-2
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2749.5	90.3	584	PIA3_MOUSE	O54714 mus musculus
3	1636.5	53.8	651	PIA1_MOUSE	O88907 mus musculus
4	1621.5	53.3	651	PIA1_HUMAN	O75925 homo sapien
5	987.5	32.4	510	PIA1_HUMAN	O8N2W9 homo sapien
6	975	32.0	507	PIAG_MOUSE	Q9Jm05 mus musculus
7	263	8.6	726	NFIL1_YEAST	Q12216 saccharomyc
8	145.5	4.8	5262	MLL2_HUMAN	O14686 homo sapien
9	142	4.7	1509	GSRI_HUMAN	Q9NZM4 homo sapien
10	133.5	4.4	1329	KF10_HUMAN	Q9P218 homo sapien
11	129.5	4.3	1822	ZAP3_HUMAN	P49750 homo sapien
12	128.5	4.2	5147	PCLO_HUMAN	Q9Y6V0 homo sapien
13	127	4.2	5038	PCLO_MOUSE	Q9GYX7 mus musculus
14	126	4.1	1152	MAP4_HUMAN	P27816 homo sapien
15	125.5	4.1	3866	HRX_MOUSE	P52200 mus musculus
16	125	4.1	893	DAG1_MOUSE	Q62165 mus musculus
17	123.5	4.1	1257	PCGN_RAT	P55067 rattus norv
18	122	4.0	895	DAG1_BOVIN	O18738 bos taurus
19	121.5	4.0	931	MRTA_HUMAN	Q969V6 homo sapien
20	121	4.0	1324	IRS2_HUMAN	Q9Y4H2 homo sapien
21	120.5	4.0	1072	MAP4_BOVIN	P36225 bos taurus
22	120	3.9	789	ATX1_RAT	Q61540 rattus norv
23	119.5	3.9	964	MRTA_MOUSE	O8K4J6 mus musculus
24	119	3.9	487	EBN2_EBV	P12978 Epstein-bar
25	119	3.9	1048	EBN2_HUMAN	O75362 homo sapien
26	118.5	3.9	1003	MD6_HUMAN	Q96dn6 homo sapien
27	118.5	3.9	1199	P121_RAT	P52591 rattus norv
28	118	3.9	1088	MRTB_HUMAN	Q9ULH7 homo sapien
29	118	3.9	1386	ZAP3_MOUSE	Q9R0I7 mus musculus
30	118	3.9	1567	FMN2_MOUSE	Q9J104 mus musculus
31	118	3.9	4911	MLL3_HUMAN	Q8NEZ4 homo sapien
32	117	3.8	1300	SAL3_HUMAN	Q9BXA9 homo sapien
33	116.5	3.8	1077	C3G_HUMAN	Q13905 homo sapien

34 116.5 3.8 1142 1 KPC1_NEUCR P87253 neurospora
35 116.5 3.8 2688 1 ZEB1_MOUSE Q03172 mus musculus
36 116.5 3.8 5179 1 MUC2_HUMAN Q02817 homo sapien
37 116 3.8 895 1 GNSD_RAT Q03386 rattus norv
38 115.5 3.8 484 1 IRX5_MOUSE Q91KQ4 mus musculus
39 115 3.8 1268 1 PCGN_MOUSE P55066 mus musculus
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41 113.5 3.7 1323 1 SAL3_MOUSE Q62255 mus musculus
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45 113 3.7 1050 1 ULK1_HUMAN O75385 homo sapien

ALIGNMENTS

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AC Q9Y6X2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RA Deika N., Saka N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIAS3).";
RL J. Hum. Genet. 44:193-196 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MYT-type zinc finger.

RX MEDLINE=2009325; PubMed=10628744;
RA Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao J.,
RA Shuai K., French F.S.;
RT "Protein inhibitor of activated STAT-1 (signal transducer and
RT activator of transcription-1) is a nuclear receptor coregulator
RT expressed in human testis";
RL Mol. Endocrinol. 14:14-26(2000).
RN [3].
RP SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=B-cell;
RX MEDLINE=97320420; PubMed=9177271;
RA Valdez B.C., Henning D., Perlick L., Busch R.K., Busch H.;
RT "Cloning and characterization of Gu/RH-II binding protein";
RL Biochem. Biophys. Res. Commun. 234:335-340(1997).
CC !- FUNCTION: Specifically inhibits activated STAT1 signaling by
CC blocking its DNA-binding activity.
CC !- SUBUNIT: Binds p53, RNA helicase II and androgen receptor.
CC !- SUBCELLULAR LOCATION: Nuclear.
CC !- TISSUE SPECIFICITY: Highly expressed in testis.
CC !- SIMILARITY: Contains 1 SAP domain.
CC !- SIMILARITY: Contains 1 MIZ-type zinc finger.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF077951; AAC36702.1; --
CC EMBL; AF167160; AAD49722.1; --
CC EMBL; U78524; AAB58488.1; --
CC Genbank; HGNC:2752; PIAS1.
CC MIM; 603566; --
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0003714; F:transcription co-repressor activity; TAS.
CC GO; GO:0007259; P:JAK-STAT cascade; TAS.
CC InterPro; IPR003034; SAP.
CC InterPro; IPR004181; ZnF_MIZ.
CC Pfam; PF02037; SAP; 1.
CC Pfam; PF02891; zf-MIZ; 1.
CC SMART; SM00513; SAP; 1.
CC PROSITE; PS00800; SAP; 1.
CC Repeat; Zinc-finger; Nuclear protein.
FT DOMAIN 11 45
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FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 577 634 SER-RICH
FT DOMAIN 520 615 4 X 4 AA REPEATS OF N-T-S-L.
FT REPEAT 520 523 1.
FT REPEAT 557 560 2.
FT REPEAT 598 601 3 (APPROXIMATE).
FT REPEAT 612 615 4 (APPROXIMATE).
FT CONFLICT 119 119 E K (IN REF. 1).
FT CONFLICT 266 268 PV -> T (IN REF. 1).
FT CONFLICT 613 613 S -> T (IN REF. 3).
SQ SEQUENCE 651 AA; 71835 MW; AA69338221124119 CRC64;

Query Match 53.3%; Score 1621.5; DB 1; Length 651;
Best Local Similarity 56.5%; Pred. No. 2.5e-98;
Matches 346; Conservative 82; Mismatches 131; Indels 53; Gaps 20;

Qy 1 MKIKELRRRFRKTLGSDLSL-----LSLPPGTSVP-----GSPSPASIPPTLL 47
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Qy 48 TPTLLGPKREYDMHPLP---QPVHPDVTMKPLPEYVGVGLIPTLLASTSSORFEEA 104
Db 109 LPVSLGPKHELEL-PLHTSALHPVHPDIKQLKPLFPYDLDELKPTSLASDNSQRFRT 167

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Db 347 RALTCSHLQCFDAILYQMEKKPTWPCVCKKAPYEHLLIIDGLFWEILLYKVCDCRIQ 406
Qy 345 FMEDGSCWCPMKPKKAESEVCPPOY-GLDGLQYS-----PVQGNQSENK-KRVEIDITI 398
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Db 465 DSSSDEEEPSAKRTPSUSPTSL--NNKGLISLPHQASPVSRTPSPDAVTSYNTS 522
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Qy 563 LTGCRSDVISLD 574
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ID PIAG_HUMAN STANDARD; PRT; 510 AA.
AC Q8N2W9; O75926; Q96G19; Q9UNI6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein gamma (PIAS-gamma)
DE (PIASy).
GN PIASG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RC TISSUE=B-cell;
RX MEDLINE=98393695; PubMed=9724754;
RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,
RA Shuai K.;
RT "Inhibition of Stat1-mediated gene activation by PIAS1";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Skin;
RX MEDLINE=23384257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.8056 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-4

Perfect score: 3056

Sequence: 1 MKIKELYRRRPRKTLGPSD.....GVLPSGSLTGCRSDIISLD 574

Scoring table: BLOSUM62

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Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3056	100.0	619	PIA3 HUMAN	Q9Y6X2 homo sapien
2	2718.5	89.0	584	PIA3 MOUSE	O54714 mus musculus
3	1627.5	53.3	651	PIA1 MOUSE	O88907 mus musculus
4	1613.5	52.8	651	PIA1 HUMAN	O75925 homo sapien
5	994.5	32.5	510	PIA3 HUMAN	Q8n2w3 homo sapien
6	976	31.9	507	PIA3 MOUSE	Q9Jm05 mus musculus
7	268.5	8.8	726	NEF1 YEAST	Q12216 saccharomyc
8	152.5	5.0	1509	GSR1 HUMAN	Q9nzm4 homo sapien
9	138.5	4.5	5262	MLL2 HUMAN	O14686 homo sapien
10	134.5	4.4	1003	MBD6 HUMAN	Q36dn6 homo sapien
11	130	4.3	638	2297 MOUSE	Q320g7 mus musculus
12	130	4.3	1152	NAP4 HUMAN	P27816 homo sapien
13	129	4.2	1300	SAL3 HUMAN	Q9bxa9 homo sapien
14	128.5	4.2	1072	NAP4 BOVIN	P36225 bos taurus
15	128.5	4.2	1134	SRE1 MOUSE	Q9wt93 mus musculus
16	125	4.1	487	EBN2 EBV	P12978 Epstein-bar
17	125	4.1	1484	CBS2 HUMAN	Q9bxf3 homo sapien
18	124.5	4.1	1329	KF10 HUMAN	Q9p218 homo sapien
19	124	4.1	579	REL8 HUMAN	Q01201 homo sapien
20	124	4.1	1844	POLR TYMV	P20128 turnip yell
21	124	4.1	5703	MUS8 HUMAN	Q9hc84 homo sapien
22	122	4.0	1516	CA1H HUMAN	P39060 homo sapien
23	122	4.0	5147	PCL0 HUMAN	Q9Y6v0 homo sapien
24	121.5	4.0	2364	PCSA BOVIN	P33608 bos taurus
25	121	4.0	1567	FMN2 MOUSE	Q9J104 mus musculus
26	120	3.9	542	ZYX CHICK	Q04584 gallus gall
27	120	3.9	1077	C3G HUMAN	Q13905 homo sapien
28	119	3.9	634	Z297 HUMAN	O15209 homo sapien
29	119	3.9	1257	PCSN RAT	P35067 rattus norv
30	119	3.9	1464	CA13 MOUSE	P08121 mus musculus
31	118	3.9	789	ATX1 RAT	Q63540 rattus norv
32	118	3.9	1574	SYJ1 RAT	Q62910 rattus norv
33	117.5	3.8	649	V70K EPMV	P20129 eggplant mo

34	117.5	3.8	2688	1	ZEPI MOUSE	Q03172 mus musculus
35	117	3.8	5038	1	PCLO MOUSE	Q9QYX7 mus musculus
36	116.5	3.8	1323	1	SAL3 MOUSE	Q62255 mus musculus
37	116.5	3.8	1822	1	ZAP3 HUMAN	P49750 homo sapien
38	116.5	3.8	1844	1	POLR TYMV	P10358 turnip yell
39	116	3.8	817	1	VRP1 YEAST	P37370 saccharomyc
40	116	3.8	895	1	GND5 RAT	Q03386 rattus norv
41	115.5	3.8	789	1	PRD1 HUMAN	O75626 homo sapien
42	115.5	3.8	3164	1	TEGU_HSV1	P10220 herpes simp
43	115	3.8	893	1	DAG1 MOUSE	Q62165 mus musculus
44	115	3.8	1132	1	BAT3 HUMAN	P46379 homo sapien
45	114.5	3.7	1844	1	POLR TYMVC	P28477 turnip yell

ALIGNMENTS

RESULT 1
PIA3 HUMAN
ID PIA3 HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIAS3).";
RL J. Hum. Genet. 44:193-196(1999).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- TISSUE SPECIFICITY: Widely expressed.
-!- SIMILARITY: Contains 1 SAP domain.
-!- SIMILARITY: Contains 1 MIZ-type zinc finger.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.55357 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-5

Perfect score: 544

Sequence: 1 TWTCPCVCDKAPVESLIIDG.....KKKVEVDLTIESSSDEEDL 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	100.0	619	1	PIA3_HUMAN
2	495	91.0	584	1	Q9Y6X2_MOUSE
3	327	60.1	651	1	PIA3_MOUSE
4	322	59.2	651	1	PIA1_MOUSE
5	257.5	47.3	510	1	PIA1_HUMAN
6	222	40.8	507	1	PIA2_MOUSE
7	92.5	17.0	726	1	NP11_YEAST
8	88.5	16.3	627	1	BA1A_XENLA
9	76	14.0	1479	1	BA1B_MOUSE
10	74.5	13.7	1025	1	CE2_MOUSE
11	73.5	13.5	765	1	KF10_MOUSE
12	72.5	13.3	469	1	CHBP_MOUSE
13	72	13.2	129	1	YN70_ARCFU
14	69.5	12.8	249	1	Q101_ARATH
15	69.5	12.8	250	1	EXPI_ARATH
16	69.5	12.8	269	1	EX23_ARATH
17	69.5	12.8	1436	1	WC11_BOVIN
18	68.5	12.6	248	1	EX15_ARATH
19	68	12.5	1556	1	BA1A_HUMAN
20	67.5	12.4	92	1	PERN_AZOFI
21	67.5	12.4	276	1	EX25_ARATH
22	67.5	12.4	462	1	MSTA_DROME
23	67.5	12.4	661	1	HT31_ARATH
24	67	12.3	230	1	YF42_METKA
25	67	12.3	235	1	YQ57_CAEEL
26	67	12.3	1453	1	CA11_CHICK
27	66.5	12.2	768	1	ITP8_RABIT
28	66	12.1	332	1	TRPD_VIBPA
29	66	12.1	526	1	HRG_RABIT
30	66	12.1	1972	1	BA2B_HUMAN
31	65	11.9	331	1	TRPD_CLOAB
32	65	11.9	851	1	CT06_HUMAN
33	65	11.9	1483	1	BA1B_HUMAN

34 65 11.9 1516 1 CALH_HUMAN
35 65 11.9 3565 1 CSML_HUMAN
36 64.5 11.9 101 1 FER_PYLIS
37 64.5 11.9 124 1 RS16_RHIME
38 64.5 11.9 5038 1 RYR1_HUMAN
39 63.5 11.7 260 1 EX16_ARATH
40 63.5 11.7 473 1 MDM2_XENLA
41 63 11.6 246 1 TLPI1_PRUPE
42 63 11.6 862 1 DCHS_MOUSE
43 63 11.6 877 1 PI01_PIG
44 63 11.6 1235 1 RNT1_ARATH
45 62.5 11.5 258 1 EXP9_ARATH

P39060 homo sapien
Q96P27 homo sapien
P81901 pyrobaculum m
Q92143 rhizobium m
P21817 homo sapien
Q9M289 arabidopsis
P56273 xenopus lae
P83332 prunus pers
P23738 mus musculus
O02696 sus scrofa
Q9FJ00 arabidopsis
Q91299 arabidopsis

ALIGNMENTS

RESULT 1
PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UF13;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9233144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIAS3).";
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AB021868; BAA78533.1; --
DR EMBL; BC001154; AAH01154.1; --
DR EMBL; BC030556; AAH30556.1; --
DR EMBL; AL122061; CAB59241.1; --
DR PIR; T34525; T34525.
DR MIM; 605987; --
DR InterPro; IPR003034; SAP.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-Miz; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Zinc-finger; Nuclear protein.
FT DOMAIN 2 36
FT ZN_FING 314 366
FT MIZ-TYPE.
SQ SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 100.0%; Score 544; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 60
DB 354 TWTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 413
QY 61 YGLDGLQVSPVGGDPSENKKKVEVDLTIESSSDEEDL 99
DB 414 YGLDGLQVSPVGGDPSENKKKVEVDLTIESSSDEEDL 452

RESULT 2

PIA3_MOUSE
ID PIA3_MOUSE STANDARD; PRT; 584 AA.
AC 054714;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049615; PubMed=9388184;
RA Chung C.D., Liao J., Rao X., Jay P., Berta P., Shuai K.;
RT "Specific" inhibition of Stat3 signal transduction by PIAS3.;
RL Science 278:1803-1805 (1997).
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
CC blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF034080; AAB88902.2; --
DR MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-Miz; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Zinc-finger; Nuclear protein.
FT DOMAIN 2 36
FT ZN_FING 279 331
FT MIZ-TYPE.
SQ SEQUENCE 584 AA; 63652 MW; 8567831ACALD0D98 CRC64;

Query Match 91.0%; Score 495; DB 1; Length 584;
Best Local Similarity 91.9%; Pred. No. 1.4e-43;
Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TWTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 60
DB 319 TWTCPVCDKKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 378
QY 61 YGLDGLQVSPVGGDPSENKKKVEVDLTIESSSDEEDL 99
DB 379 YGLDGLQVSPVGGDPSENKKKVEVDLTIESSSDEEDL 417

RESULT 3

PIA1_MOUSE
ID PIA1_MOUSE STANDARD; PRT; 651 AA.
AC 086007;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1).
DE protein 1).
GN PIAS1 OR DEADBP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=98393695; PubMed=9724754;
RA Liu B., Liao J., Rao X., Mushner S.A., Chung C.D., Chang D.D.,
RA Shuai K.;
RT "Inhibition of Stat1-mediated gene activation by PIAS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631 (1998).
CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
CC blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF077950; AAC36701.1; --
DR MGD; MGI:1913125; Pias1.
DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-Miz; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Repeat; Zinc-finger; Nuclear protein.
FT DOMAIN 11 45
FT ZN_FING 331 383
FT MIZ-TYPE.
FT DOMAIN 56 64
FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.754 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-6

Perfect score: 2943

Sequence: 1 MKIKELVRRFPKTLGPSD.....GPLPSPGSLTGCSDIXSLD 572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2816	95.7	619	1	PIA3_HUMAN
2	2573.5	87.4	584	1	Q54714 mus musculus
3	1488.5	50.6	651	1	PIA1_MOUSE
4	1480.5	50.3	651	1	PIA1_HUMAN
5	893	30.3	510	1	PIA2_HUMAN
6	881.5	30.0	507	1	PIA2_MOUSE
7	204	6.9	726	1	NP11_YEAST
8	141	4.8	1509	1	GSR1_HUMAN
9	130.5	4.4	1329	1	KP10_HUMAN
10	120	4.1	893	1	DAG1_MOUSE
11	119.5	4.1	1088	1	MR1B_HUMAN
12	119	4.0	1300	1	SAL3_HUMAN
13	118	4.0	895	1	DAG1_BOVIN
14	118	4.0	895	1	DAG1_HUMAN
15	117	4.0	1567	1	PMN2_MOUSE
16	116.5	4.0	1257	1	PCGN_RAT
17	116	3.9	2063	1	NC06_HUMAN
18	115	3.9	487	1	EBN2_EBV
19	114.5	3.9	1072	1	MAP4_BOVIN
20	113.5	3.9	542	1	ZYX_CHICK
21	113.5	3.9	1574	1	SYJ1_RAT
22	113	3.8	5262	1	MLL2_HUMAN
23	112	3.8	2364	1	PGC4_BOVIN
24	112	3.8	3866	1	HRX_MOUSE
25	111	3.8	3164	1	TEGU_HSV1
26	110.5	3.8	852	1	WS14_HUMAN
27	110	3.7	895	1	DAG1_RABIT
28	110	3.7	1516	1	CALH_HUMAN
29	109.5	3.7	1003	1	MBD6_HUMAN
30	109.5	3.7	1142	1	KPCI_NEOCR
31	108.5	3.7	789	1	ATX1_RAT
32	108.5	3.7	901	1	A180_MOUSE
33	108.5	3.7	5179	1	MUC2_HUMAN

ALIGNMENTS

RESULT 1

PIA3_HUMAN
ID PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92253144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT Isolation and chromosomal assignment of a human gene encoding protein
RT inhibitor of activated STAT3 (PIA3).
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast Cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
RA Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
CC blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear [by similarity].
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MTZ-type zinc finger.

34 108.5 3.7 5703 1 MUSB_HUMAN Q9hc84 homo sapien
35 107 3.6 1152 1 MAP4_HUMAN P27816 homo sapien
36 107 3.6 1324 1 IRS2_MOUSE Q9y4h2 homo sapien
37 107 3.6 5038 1 PCLO_MOUSE Q9gyx7 mus musculus
38 107 3.6 5147 1 PCLO_MOUSE Q9y6v0 homo sapien
39 106.5 3.6 1812 1 BRC1_MOUSE P48754 mus musculus
40 106 3.6 634 1 Z297_HUMAN O15209 homo sapien
41 106 3.6 639 1 SF01_HUMAN Q15637 homo sapien
42 106 3.6 3859 1 TRAP_HUMAN Q9y4a5 homo sapien
43 105.5 3.6 1321 1 IRS2_MOUSE P81122 mus musculus
44 105.5 3.6 1822 1 ZAP3_HUMAN P49750 homo sapien
45 105 3.6 936 1 MRTA_XENLA Q8ayc2 xenopus lae

[illegible]

```

RESULT 4
PIAL HUMAN
ID PIAL HUMAN STANDARD; PRT; 651 AA.
AC O75925; Q9UN02;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 1 (Gu binding protein)
DE (GBP) (RNA helicase II binding protein) (DEAD/H box-binding protein
DE 1).
PIAS1 OR DDXEPL.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND FUNCTION.
RP TISSUE=B-cell;
RC MEDLINE=98393695; PubMed=9724754;
RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,
RA Shuai K.;
RP "Inhibition of Stat1-mediated gene activation by PIAS1.";
RL "Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
[2]
RN SEQUENCE FROM N.A.
RP

```


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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.55357 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-7

Perfect score: 543

Sequence: 1 TWTCPCVCKKAPYESLIIDG.....KKRVEVIDLTIESSSDEEDL 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	517	95.2	619	PIA3_HUMAN	Q96X22 homo sapien
2	516	95.0	584	PIA3_MOUSE	Q54714 mus musculus
3	332	61.1	651	PIA1_MOUSE	O88907 mus musculus
4	324	59.7	651	PIA1_HUMAN	O75925 homo sapien
5	251.5	46.3	510	PIA2_HUMAN	Q82W93 homo sapien
6	218	40.1	507	PIA2_MOUSE	Q9Jm05 mus musculus
7	95	17.5	726	PIA1_YEAST	Q12216 saccharomyc
8	91.5	16.9	627	BAL1_XENLA	Q8UVF5 xenopus lae
9	79.5	14.6	469	C4BP_MOUSE	P08607 mus musculus
10	76.5	14.1	462	MSTA_DROME	O46040 drosophila
11	75	13.8	1556	BAL1_HUMAN	Q9NR12 h bromodoma
12	74	13.6	1479	BAL1_MOUSE	Q9Z277 mus musculus
13	72.5	13.4	765	PIF10_MOUSE	Q923P0 mus musculus
14	72	13.3	651	YIRF_SCHPO	Q9P713 schizosacch
15	71	13.1	129	YN70_ARCFU	O30300 archaeoglob
16	70.5	13.0	269	CR23_ARATH	Q9FL79 arabidopsis
17	70.5	13.0	1025	CR2_MOUSE	P19070 mus musculus
18	69.5	12.8	249	EX10_ARATH	Q9LDR9 arabidopsis
19	69.5	12.8	250	EX10_MOUSE	Q9C554 arabidopsis
20	69.5	12.8	881	PHFE_MOUSE	Q9D4H9 mus musculus
21	68.5	12.6	248	EX15_ARATH	O80622 arabidopsis
22	68.5	12.6	276	EX25_ARATH	Q9FL77 arabidopsis
23	68.5	12.6	661	HT31_ARATH	Q04996 arabidopsis
24	67	12.3	888	PHFE_HUMAN	Q94880 homo sapien
25	65.5	12.1	101	FER_PYRIS	P19101 pyrobaculum
26	65.5	12.1	5038	RYR1_HUMAN	P21817 homo sapien
27	65	12.0	335	FAH1_BACTN	Q8AB18 bacteroides
28	65	12.0	5037	RYR1_RABIT	P11716 oryctolagus
29	64.5	11.9	92	FERN_AZOVI	P11054 azotobacter
30	64.5	11.9	1483	BAL1_HUMAN	Q9U190 homo sapien
31	64	11.8	538	RB55_HUMAN	Q15291 homo sapien
32	64	11.8	1227	PR16_HUMAN	Q92620 homo sapien
33	64	11.8	3565	CSM1_HUMAN	Q96PZ7 homo sapien

34	63.5	11.7	260	1	EX16_ARATH	Q9M2S9 arabidopsis
35	63	11.6	519	1	IKAR_HUMAN	Q13422 homo sapien
36	63	11.6	543	1	SUW2_HUMAN	Q86YH2 homo sapien
37	63	11.6	877	1	PI01_PIG	O02696 sus scrofa
38	63	11.6	1173	1	TSPI_XENLA	P35448 xenopus lae
39	63	11.6	4911	1	MLL3_HUMAN	Q9NEZ4 homo sapien
40	62.5	11.5	258	1	EXP9_ARATH	Q9LZ99 arabidopsis
41	62.5	11.5	262	1	EXP3_ARATH	O80932 arabidopsis
42	62.5	11.5	291	1	ZUP1_CAMJE	Q9PIN2 campylobact
43	62.5	11.5	303	1	ATNB_CANFA	P06583 canis famil
44	62.5	11.5	326	1	PDLI_MOUSE	O70400 mus musculu
45	62.5	11.5	731	1	CND2_MOUSE	Q8C156 mus musculu

ALIGNMENTS

RESULT 1
PIA3_HUMAN
ID PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q96X22; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99253144; PubMed=10319586;
RA Ueki N., Oishi N., Yano K., Saito I., Masuho Y., Muramatsu M.;
RT Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIAS3).
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22398257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AB021868; BAA78533.1; --
 EMBL; BC001154; AAH01154.1; --
 EMBL; BC030556; AAH30556.1; --
 EMBL; AL122061; CAB59241.1; --
 PIR; T34525; T34525.
 MIM; 605987; --
 InterPro; IPR003034; SAP.
 InterPro; IPR004181; Znf_MIZ.
 Pfam; PF02037; SAP; 1.
 Pfam; PF02891; zf-MIZ; 1.
 SMART; SM00513; SAP; 1.
 PROSITE; PS05080; SAP; 1.
 Zinc-finger; Nuclear protein.
 DOMAIN 2 36
 ZN_FING 314 366 MIZ-TYPE.
 SQ SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 95.2%; Score 517; DB 1; Length 619;
 Best Local Similarity 94.9%; Pred. No. 3.6e-46;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TWTCPCVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
 DB 354 TWTCPCVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 413

QY 61 YGLDGLQYSPVQEGNQSENKKRVEVDLTITSSSDEEDL 99
 DB 414 YGLDGLQYSPVQEGNQSENKKRVEVDLTITSSSDEEDL 452

RESULT 2

PIA3_MOUSE
 ID PIA3_MOUSE STANDARD; PRT; 584 AA.
 AC 054714;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 3.
 GN PIAS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049615; PubMed=9388184;
 RA Chung C.D., Liao J., Rao X., Jay P., Berta P., Shuai K.;
 RT Specific inhibition of Stat3 signal transduction by PIAS3.;
 RL Science 278:1803-1805 (1997).
 CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AF034080; AAB88902.2; --
 MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS05080; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 ZN_FING 279 331 MIZ-TYPE.
 SQ SEQUENCE 584 AA; 63652 MW; 8567831ACA1D0D98 CRC64;

Query Match 95.0%; Score 516; DB 1; Length 584;
 Best Local Similarity 96.0%; Pred. No. 4.3e-46;
 Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TWTCPCVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
 DB 319 TWTCPCVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 378

QY 61 YGLDGLQYSPVQEGNQSENKKRVEVDLTITSSSDEEDL 99
 DB 379 YGLDGLQYSPVQEGNQSENKKRVEVDLTITSSSDEEDL 417

RESULT 3

PIA1_MOUSE
 ID PIA1_MOUSE STANDARD; PRT; 651 AA.
 AC 089907;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding
 DE protein 1).
 GN PIAS1 OR DDX41.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=B-Cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kashner S.A., Chung C.D., Chang D.D.,
 RA Shuai K.;
 RT Inhibition of Stat1-mediated gene activation by PIAS1.;
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631 (1998).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AF077950; AAC36701.1; --
 MGD; MGI:1913125; Pias1.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS05080; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 ZN_FING 331 383 MIZ-TYPE.
 FT DOMAIN 56 64
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.52778 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-10

Perfect score: 517

Sequence: 1 WTCFVCDKAPYSLIDGL.....KKXVEVDLTIESSDDEDL 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	97.7	619	PIA3 HUMAN	Q9Y6X2 homo sapien
2	478	92.5	584	PIA3 MOUSE	O54714 mus musculus
3	314	60.7	651	PIA1 MOUSE	O88907 mus musculus
4	309	59.8	651	PIA1 HUMAN	O75925 homo sapien
5	234.5	45.4	510	PIA2 HUMAN	Q8n2w9 homo sapien
6	214	41.4	507	PIA2 MOUSE	Q9Ym05 mus musculus
7	87.5	16.9	726	NPII YEAST	Q12216 saccharomyc
8	81.5	15.8	627	BA1A XENLA	Q8uvr5 xenopus lae
9	70	13.5	469	CABP MOUSE	P08607 mus musculus
10	67	13.0	1479	BA1B MOUSE	Q9z277 mus musculus
11	66.5	12.9	92	FRN1 AZOVI	P11054 azotobacter
12	65.5	12.7	1436	WC11 BOVIN	P30205 bos taurus
13	65	12.6	538	REB5 HUMAN	Q15291 homo sapien
14	64.5	12.5	249	EX10 ARATH	Q91d99 arabidopsis
15	64.5	12.5	250	EXPI ARATH	Q9c554 arabidopsis
16	64.5	12.5	269	EX23 ARATH	O9f179 arabidopsis
17	64.5	12.5	765	KE10 MOUSE	Q923p0 mus musculus
18	64	12.4	995	CG1A DROME	Q9ngc3 drosophila
19	64	12.4	1905	TAGB DICDI	P54683 dictyosteli
20	63.5	12.3	248	EX15 ARATH	O80622 arabidopsis
21	63.5	12.3	335	FAH1 BACTN	Q8ab18 bacteroides
22	63.5	12.3	754	ASPH BOVIN	Q28056 bos taurus
23	63	12.2	3565	CSM1 HUMAN	Q96p27 homo sapien
24	62.5	12.1	276	EX25 ARATH	Q9f177 arabidopsis
25	62.5	12.1	661	HT31 ARATH	Q04996 arabidopsis
26	62.5	12.1	1025	C321 MOUSE	P19070 mus musculus
27	62	12.0	172	PRP2 RAT	P10164 rattus norv
28	61.5	11.9	5038	RYR1 HUMAN	P21817 homo sapien
29	61	11.8	230	YF42 METKA	Q8cv58 methanopyru
30	60.5	11.7	428	SMY3 HUMAN	Q9f7b4 homo sapien
31	60.5	11.7	610	DRTS TOXGO	Q07422 toxoplasma
32	60	11.6	539	CH60 FUSNN	Q8f5x7 fusobacteri
33	60	11.6	591	UN18 CAEEL	P34815 caenorhabdi

ALIGNMENTS

RESULT 1									
PIA3_HUMAN									
ID	PIA3_HUMAN	STANDARD;	PRT;	619	AA.				
AC	Q9Y6X2; Q9UF13;								
DT	28-FEB-2003 (Rel. 41, Created)								
DT	28-FEB-2003 (Rel. 41, Last sequence update)								
DT	10-OCT-2003 (Rel. 42, Last annotation update)								
DE	Protein inhibitor of activated STAT protein 3.								
GN	PIA33								
OS	Homo sapiens (Human)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=9253144; PubMed=10319586;								
RT	Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;								
RT	"Isolation and chromosomal assignment of a human gene encoding protein								
RT	inhibitor of activated STAT3 (PIA33).";								
RL	J. Hum. Genet. 44:193-196(1999).								
RN	[2];								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Blood, and Muscle;								
RX	MEDLINE=22388257; PubMed=12477932;								
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,								
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,								
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,								
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,								
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,								
RA	Butterfield Y.S.N., Kryzyski M.I., Skalska U., Smalusz D.E.,								
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;								
RT	"Generation and initial analysis of more than 15,000 full-length								
RT	human and mouse cDNA sequences.";								
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).								
RN	[3];								
RP	SEQUENCE OF 301-619 FROM N.A.								
RC	TISSUE=Breast cancer;								
RA	Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;								
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.								
CC	-!- FUNCTION: Specifically inhibits activated STAT3 signaling by								
CC	blocking its DNA-binding activity. (By similarity).								
CC	-!- SUBCELLULAR LOCATION: Nuclear (By similarity).								
CC	-!- TISSUE SPECIFICITY: Widely expressed.								
CC	-!- SIMILARITY: Contains 1 SAP domain.								
CC	-!- SIMILARITY: Contains 1 MIZ-type zinc finger.								

Q9fjr0 arabidopsis
P15208 mus musculus
P15127 rattus norv
O14129 schizosacch
O46040 drosophila
P44884 haemophilus
Q28640 oryctolagus
Q26013 oryctolagus
O51056 borrelia bu
Q12094 saccharomyc
Q9hz68 pseudomonas
P09309 varicella-z

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DR EMBL; AB021868; BAA78533.1; -
 DR EMBL; BC001154; AAH01154.1; -
 DR EMBL; BC030556; AAH30556.1; -
 DR EMBL; AL122061; CAB59241.1; -
 DR PIR; T34525; T34525.
 DR MIM; 605987; -
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 FT ZN_FING 314 366 MIZ-TYPE.
 SQ SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 97.7%; Score 505; DB 1; Length 619;
 Best Local Similarity 94.9%; Pred. No. 1.3e-48;
 Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WTCPCVCDKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPPGY 60
 DB 355 WTCPCVCDKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPPGY 414

QY 61 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 98
 DB 415 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 452

RESULT 2
 PIA3 MOUSE
 ID PIA3_MOUSE STANDARD; PRT; 584 AA.
 AC 054714;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Protein inhibitor of activated STAT protein 3.
 GN PIAS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049615; PubMed=9388184;
 RA Chung C.D., Liao J., Rao X., Jay P., Berta P., Shuai K.;
 RT "Specific inhibition of Stat3 signal transduction by PIAS3.";
 RL Science 278:1803-1805 (1997)
 CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF034080; AAB89902.2; -
 DR MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 FT ZN_FING 279 331 MIZ-TYPE.
 SQ SEQUENCE 584 AA; 63652 MW; 8567831ACALDOD98 CRC64;

Query Match 92.5%; Score 478; DB 1; Length 584;
 Best Local Similarity 90.8%; Pred. No. 1.3e-45;
 Matches 89; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 WTCPCVCDKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPPGY 60
 DB 320 WTCPCVCDKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPPGY 379

QY 61 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 98
 DB 380 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 417

RESULT 3
 PIA1 MOUSE
 ID PIA1_MOUSE STANDARD; PRT; 651 AA.
 AC Q88907;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1).
 GN PIAS1 OR NXPB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=B-cell;
 RC MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D., Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIAS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631 (1998).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF077950; AAC36701.1; -
 DR MGD; MGI:1913125; Piasl.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 FT ZN_FING 331 383 MIZ-TYPE.
 FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).